



SEQUENCE LISTING

<110> John P. Cerulli et al.

<120> REGULATING LIPID LEVELS VIA THE ZMAX1 or HBM GENE

<130> 032796-019

<150> Unassigned

<151> 2000-05-26

<150> US 09/543,771

<151> 2000-04-05

<150> US 09/544,398

<151> 2000-04-05

<160> 62

<210> 1

<211> 5120

<212> DNA

<213> Homo sapiens

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Met Glu Ala Ala Pro Pro Gly Pro Pro Trp Pro Leu Leu
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Leu Leu Leu Leu Leu Leu Ala Leu Cys Gly Cys Pro Ala Pro Ala
15 20 25
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Ala Ala Ser Pro Leu Leu Leu Phe Ala Asn Arg Arg Asp Val Arg Leu

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gtg gac gcc ggc gga gtc aag ctg gag tcc acc atc gtg gtc agc ggc				253
Val Asp Ala Gly Gly Val Lys Leu Glu Ser Thr Ile Val Val Ser Gly				
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ctg gag gat gcg gcc gca gtg gac ttc cag ttt tcc aag gga gcc gtg				301
Leu Glu Asp Ala Ala Ala Val Asp Phe Gln Phe Ser Lys Gly Ala Val				
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Tyr Trp Thr Asp Val Ser Glu Glu Ala Ile Lys Gln Thr Tyr Leu Asn				
80	85	90		
cag acg ggg gcc gcc gtg cag aac gtg gtc atc tcc ggc ctg gtc tct				397
Gln Thr Gly Ala Ala Val Gln Asn Val Val Ile Ser Gly Leu Val Ser				
95	100	105		
ccc gac ggc ctc gcc tgc gac tgg gtg ggc aag aag ctg tac tgg acg				445
Pro Asp Gly Leu Ala Cys Asp Trp Val Gly Lys Lys Leu Tyr Trp Thr				
110	115	120	125	
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Asp Ser Glu Thr Asn Arg Ile Glu Val Ala Asn Leu Asn Gly Thr Ser				
130	135	140		
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Arg Lys Val Leu Phe Trp Gln Asp Leu Asp Gln Pro Arg Ala Ile Ala				
145	150	155		
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Leu Asp Pro Ala His Gly Tyr Met Tyr Trp Thr Asp Trp Gly Glu Thr				
160	165	170		
ccc cgg att gag cgg gca ggg atg gat ggc agc acc cgg aag atc att				637
Pro Arg Ile Glu Arg Ala Gly Met Asp Gly Ser Thr Arg Lys Ile Ile				
175	180	185		
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Val Asp Ser Asp Ile Tyr Trp Pro Asn Gly Leu Thr Ile Asp Leu Glu	
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Glu Gln Lys Leu Tyr Trp Ala Asp Ala Lys Leu Ser Phe Ile His Arg	
210	220
gcc aac ctg gac ggc tcg ttc cgg cag aag gtg gtg gag ggc agc ctg	781
Ala Asn Leu Asp Gly Ser Phe Arg Gln Lys Val Val Glu Gly Ser Leu	
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Thr His Pro Phe Ala Leu Thr Leu Ser Gly Asp Thr Leu Tyr Trp Thr	
240	250
gac tgg cag acc cgc tcc atc cat gcc tgc aac aag cgc act ggg ggg	877
Asp Trp Gln Thr Arg Ser Ile His Ala Cys Asn Lys Arg Thr Gly Gly	
255	265
aag agg aag gag atc ctg agt gcc ctc tac tca ccc atg gac atc cag	925
Lys Arg Lys Glu Ile Leu Ser Ala Leu Tyr Ser Pro Met Asp Ile Gln	
270	285
gtg ctg agc cag gag cgg cag cct ttc ttc cac act cgc tgt gag gag	973
Val Leu Ser Gln Glu Arg Gln Pro Phe Phe His Thr Arg Cys Glu Glu	
290	300
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1021	
Asp Asn Gly Gly Cys Ser His Leu Cys Leu Leu Ser Pro Ser Glu Pro	
305	315
ttc tac aca tgc gcc tgc ccc acg ggt gtg cag ctg cag gac aac ggc	
1069	
Phe Tyr Thr Cys Ala Cys Pro Thr Gly Val Gln Leu Gln Asp Asn Gly	
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agg acg tgt aag gca gga gcc gag gag gtg ctg ctg ctg gcc cgg cgg	
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Arg Thr Cys Lys Ala Gly Ala Glu Glu Val Leu Leu Leu Ala Arg Arg

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1165

Thr Asp Leu Arg Arg Ile Ser Leu Asp Thr Pro Asp Phe Thr Asp Ile

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360

365

gtg ctg cag gtg gac gac atc cgg cac gcc att gcc atc gac tac gac
1213

Val Leu Gln Val Asp Asp Ile Arg His Ala Ile Ala Ile Asp Tyr Asp

370

375

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ccg cta gag ggc tat gtc tac tgg aca gat gac gag gtg cgg gcc atc
1261

Pro Leu Glu Gly Tyr Val Tyr Trp Thr Asp Asp Glu Val Arg Ala Ile

385

390

395

cgc agg gcg tac ctg gac ggg tct ggg gcg cag acg ctg gtc aac acc
1309

Arg Arg Ala Tyr Leu Asp Gly Ser Gly Ala Gln Thr Leu Val Asn Thr

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405

410

gag atc aac gac ccc gat ggc atc gcg gtc gac tgg gtg gcc cga aac
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Glu Ile Asn Asp Pro Asp Gly Ile Ala Val Asp Trp Val Ala Arg Asn

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ctc tac tgg acc gac acg ggc acg gac cgc atc gag gtg acg cgc ctc
1405

Leu Tyr Trp Thr Asp Thr Gly Thr Asp Arg Ile Glu Val Thr Arg Leu

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440

445

aac ggc acc tcc cgc aag atc ctg gtg tcg gag gac ctg gac gag ccc
1453

Asn Gly Thr Ser Arg Lys Ile Leu Val Ser Glu Asp Leu Asp Glu Pro

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455

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cga gcc atc gca ctg cac ccc gtg atg ggc ctc atg tac tgg aca gac
1501

Arg Ala Ile Ala Leu His Pro Val Met Gly Leu Met Tyr Trp Thr Asp

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475

tgg gga gag aac cct aaa atc gag tgt gcc aac ttg gat ggg cag gag
1549

Trp Gly Glu Asn Pro Lys Ile Glu Cys Ala Asn Leu Asp Gly Gln Glu

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490

cgg cgt gtg ctg gtc aat gcc tcc ctc ggg tgg ccc aac ggc ctg gcc
1597

Arg Arg Val Leu Val Asn Ala Ser Leu Gly Trp Pro Asn Gly Leu Ala

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ctg gac ctg cag gag ggg aag ctc tac tgg gga gac gcc aag aca gac
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Leu Asp Leu Gln Glu Gly Lys Leu Tyr Trp Gly Asp Ala Lys Thr Asp

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515

520

525

aag atc gag gtg atc aat gtt gat ggg acg aag agg cgg acc ctc ctg
1693

Lys Ile Glu Val Ile Asn Val Asp Gly Thr Lys Arg Arg Thr Leu Leu

530

535

540

gag gac aag ctc ccg cac att ttc ggg ttc acg ctg ctg ggg gac ttc
1741

Glu Asp Lys Leu Pro His Ile Phe Gly Phe Thr Leu Leu Gly Asp Phe

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atc tac tgg act gac tgg cag cgc cgc agc atc gag cgg gtg cac aag
1789

Ile Tyr Trp Thr Asp Trp Gln Arg Arg Ser Ile Glu Arg Val His Lys

560

565

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1837

Val Lys Ala Ser Arg Asp Val Ile Ile Asp Gln Leu Pro Asp Leu Met

575

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1885

Gly Leu Lys Ala Val Asn Val Ala Lys Val Val Gly Thr Asn Pro Cys

590

595

600

605

gcg gac agg aac ggg ggg tgc agc cac ctg tgc ttc ttc aca ccc cac
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Ala Asp Arg Asn Gly Gly Cys Ser His Leu Cys Phe Phe Thr Pro His

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615

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gca acc cgg tgt ggc tgc ccc atc ggc ctg gag ctg ctg agt gac atg
1981

Ala Thr Arg Cys Gly Cys Pro Ile Gly Leu Glu Leu Leu Ser Asp Met

625

630

635

aag acc tgc atc gtg cct gag gcc ttc ttg gtc ttc acc agc aga gcc
2029

Lys Thr Cys Ile Val Pro Glu Ala Phe Leu Val Phe Thr Ser Arg Ala

640

645

650

gcc atc cac agg atc tcc ctc gag acc aat aac aac gac gtg gcc atc
2077

Ala Ile His Arg Ile Ser Leu Glu Thr Asn Asn Asn Asp Val Ala Ile

655

660

665

ccg ctc acg ggc gtc aag gag gcc tca gcc ctg gac ttt gat gtg tcc
2125

Pro Leu Thr Gly Val Lys Glu Ala Ser Ala Leu Asp Phe Asp Val Ser

670

675

680

685

aac aac cac atc tac tgg aca gac gtc agc ctg aag acc atc agc cgc
2173

Asn Asn His Ile Tyr Trp Thr Asp Val Ser Leu Lys Thr Ile Ser Arg

690

695

700

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2221

- Ala Phe Met Asn Gly Ser Ser Val Glu His Val Val Glu Phe Gly Leu

705

710

715

gac tac ccc gag ggc atg gcc gtt gac tgg atg ggc aag aac ctc tac
2269

Asp Tyr Pro Glu Gly Met Ala Val Asp Trp Met Gly Lys Asn Leu Tyr

720

725

730

tgg gcc gac act ggg acc aac aga atc gaa gtg gcg cgg ctg gac ggg
2317

Trp Ala Asp Thr Gly Thr Asn Arg Ile Glu Val Ala Arg Leu Asp Gly

735

740

745

cag ttc cgg caa gtc ctc gtg tgg agg gac ttg gac aac ccg agg tcg
2365

Gln Phe Arg Gln Val Leu Val Trp Arg Asp Leu Asp Asn Pro Arg Ser

750

755

760

765

ctg gcc ctg gat ccc acc aag ggc tac atc tac tgg acc gag tgg ggc
2413

Leu Ala Leu Asp Pro Thr Lys Gly Tyr Ile Tyr Trp Thr Glu Trp Gly

770

775

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ggc aag ccg agg atc gtg cgg gcc ttc atg gac ggg acc aac tgc atg
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Gly Lys Pro Arg Ile Val Arg Ala Phe Met Asp Gly Thr Asn Cys Met

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790

795

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2509

Thr Leu Val Asp Lys Val Gly Arg Ala Asn Asp Leu Thr Ile Asp Tyr

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805

810

gct gac cag cgc ctc tac tgg acc gac ctg gac acc aac atg atc gag
2557

Ala Asp Gln Arg Leu Tyr Trp Thr Asp Leu Asp Thr Asn Met Ile Glu

815

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2605

Ser Ser Asn Met Leu Gly Gln Glu Arg Val Val Ile Ala Asp Asp Leu

830

835

840

845

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2653

Pro His Pro Phe Gly Leu Thr Gln Tyr Ser Asp Tyr Ile Tyr Trp Thr

850

855

860

gac tgg aat ctg cac agc att gag cgg gcc gac aag act agc ggc cgg
2701

Asp Trp Asn Leu His Ser Ile Glu Arg Ala Asp Lys Thr Ser Gly Arg

865

870

875

aac cgc acc ctc atc cag ggc cac ctg gac ttc gtg atg gac atc ctg
2749

Asn Arg Thr Leu Ile Gln Gly His Leu Asp Phe Val Met Asp Ile Leu

880

885

890

gtg ttc cac tcc tcc cgc cag gat ggc ctc aat gac tgt atg cac aac
2797

Val Phe His Ser Ser Arg Gln Asp Gly Leu Asn Asp Cys Met His Asn

895

900

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aac ggg cag tgt ggg cag ctg tgc ctt gcc atc ccc ggc ggc cac cgc
2845

Asn Gly Gln Cys Gly Gln Leu Cys Leu Ala Ile Pro Gly Gly His Arg

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915

920

925

tgc ggc tgc gcc tca cac tac acc ctg gac ccc agc agc cgc aac tgc
2893

Cys Gly Cys Ala Ser His Tyr Thr Leu Asp Pro Ser Ser Arg Asn Cys

930

935

940

agc cgc ccc acc acc ttc ttg ctg ttc agc cag aaa tct gcc atc agt
2941

Ser Pro Pro Thr Thr Phe Leu Leu Phe Ser Gln Lys Ser Ala Ile Ser

945

950

955

· cgg atg atc ccg gac gac cag cac agc ccg gat ctc atc ctg ccc ctg
2989

· Arg Met Ile Pro Asp Asp Gln His Ser Pro Asp Leu Ile Leu Pro Leu

960

965

970

cat gga ctg agg aac gtc aaa gcc atc gac tat gac cca ctg gac aag
3037

His Gly Leu Arg Asn Val Lys Ala Ile Asp Tyr Asp Pro Leu Asp Lys

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980

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3085

Phe Ile Tyr Trp Val Asp Gly Arg Gln Asn Ile Lys Arg Ala Lys Asp
990 995 1000 1005

gac ggg acc cag ccc ttt gtt ttg acc tct ctg agc caa ggc caa aac
3133

Asp Gly Thr Gln Pro Phe Val Leu Thr Ser Leu Ser Gln Gly Gln Asn
1010 1015 1020

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Pro Asp Arg Gln Pro His Asp Leu Ser Ile Asp Ile Tyr Ser Arg Thr
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Leu Phe Trp Thr Cys Glu Ala Thr Asn Thr Ile Asn Val His Arg Leu
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Ser Gly Glu Ala Met Gly Val Val Leu Arg Gly Asp Arg Asp Lys Pro
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3325

Arg Ala Ile Val Val Asn Ala Glu Arg Gly Tyr Leu Tyr Phe Thr Asn
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Glu Arg Glu Val Leu Phe Thr Thr Gly Leu Ile Arg Pro Val Ala Leu
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Val Val Asp Asn Thr Leu Gly Lys Leu Phe Trp Val Asp Ala Asp Leu
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Lys Arg Ile Glu Ser Cys Asp Leu Ser Gly Ala Asn Arg Leu Thr Leu
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3661

Lys Thr Thr Gly Asp Lys Arg Thr Arg Ile Gln Gly Arg Val Ala His
1185 1190 1195

ctc act ggc atc cat gca gtg gag gaa gtc agc ctg gag gag ttc tca
3709

Leu Thr Gly Ile His Ala Val Glu Glu Val Ser Leu Glu Glu Phe Ser
1200 1205 1210

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3757

Ala His Pro Cys Ala Arg Asp Asn Gly Gly Cys Ser His Ile Cys Ile
1215 1220 1225

gcc aag ggt gat ggg aca cca cgg tgc tca tgc cca gtc cac ctc gtg
3805

Ala Lys Gly Asp Gly Thr Pro Arg Cys Ser Cys Pro Val His Leu Val
1230 1235 1240 1245

ctc ctg cag aac ctg ctg acc tgt gga gag ccg ccc acc tgc tcc ccg
3853

Leu Leu Gln Asn Leu Leu Thr Cys Gly Glu Pro Pro Thr Cys Ser Pro

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1270

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Trp Arg Cys Asp Gly Phe Pro Glu Cys Asp Asp Gln Ser Asp Glu Glu

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1305

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Cys Val Asp Leu Arg Leu Arg Cys Asp Gly Glu Ala Asp Cys Gln Asp

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1320

1325

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1335

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1375

1380

1385

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Val Ile Gly Ile Ile Leu Ser Leu Phe Val Met Gly Gly Val Tyr Phe

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1395

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Gly Lys Ser Met Met Ser Ser Val Ser Leu Met Gly Gly Arg Gly Gly

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1465

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1470

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4573

Ser Ser Ser Thr Lys Ala Thr Leu Tyr Pro Pro Ile Leu Asn Pro Pro

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1495

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4621

Pro Ser Pro Ala Thr Asp Pro Ser Leu Tyr Asn Met Asp Met Phe Tyr

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1545

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Ser Asp Tyr Ser Ala Ser Arg Trp Lys Ala Ser Lys Tyr Tyr Leu Asp

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1555

1560

1565

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Leu Asn Ser Asp Ser Asp Pro Tyr Pro Pro Pro Pro Thr Pro His Ser

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Gln Tyr Leu Ser Ala Glu Asp Ser Cys Pro Pro Ser Pro Ala Thr Glu

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1595

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Arg Ser Tyr Phe His Leu Phe Pro Pro Pro Pro Ser Pro Cys Thr Asp

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1605

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4965

Ser Ser

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<213> Homo sapiens

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Met Glu Ala Ala Pro Pro Gly Pro Pro Trp Pro Leu Leu

1 5 10

ctg ctg ctg ctg ctg ctg ctg gcg ctg tgc ggc tgc ccg gcc ccc gcc 157

Leu Leu Leu Leu Leu Leu Leu Ala Leu Cys Gly Cys Pro Ala Pro Ala

15 20 25

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Ala Ala Ser Pro Leu Leu Leu Phe Ala Asn Arg Arg Asp Val Arg Leu

30 35 40 45

gtg gac gcc ggc gga gtc aag ctg gag tcc acc atc gtg gtc agc ggc 253

Val Asp Ala Gly Gly Val Lys Leu Glu Ser Thr Ile Val Val Ser Gly

50 55 60

ctg gag gat gcg gcc gca gtg gac ttc cag ttt tcc aag gga gcc gtg 301

Leu Glu Asp Ala Ala Ala Val Asp Phe Gln Phe Ser Lys Gly Ala Val

65 70 75

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Tyr Trp Thr Asp Val Ser Glu Glu Ala Ile Lys Gln Thr Tyr Leu Asn	
80 85 90	
cag acg ggg gcc gcc gtg cag aac gtg gtc atc tcc ggc ctg gtc tct	397
Gln Thr Gly Ala Ala Val Gln Asn Val Val Ile Ser Gly Leu Val Ser	
95 100 105	
ccc gac ggc ctc gcc tgc gac tgg gtg ggc aag aag ctg tac tgg acg	445
Pro Asp Gly Leu Ala Cys Asp Trp Val Gly Lys Lys Leu Tyr Trp Thr	
110 115 120 125	
gac tca gag acc aac cgc atc gag gtg gcc aac ctc aat ggc aca tcc	493
Asp Ser Glu Thr Asn Arg Ile Glu Val Ala Asn Leu Asn Gly Thr Ser	
130 135 140	
cgg aag gtg ctc ttc tgg cag gac ctt gac cag ccg agg gcc atc gcc	541
Arg Lys Val Leu Phe Trp Gln Asp Leu Asp Gln Pro Arg Ala Ile Ala	
145 150 155	
ttg gac ccc gct cac ggg tac atg tac tgg aca gac tgg gtt gag acg	589
Leu Asp Pro Ala His Gly Tyr Met Tyr Trp Thr Asp Trp Val Glu Thr	
160 165 170	
ccc cgg att gag cgg gca ggg atg gat ggc agc acc cgg aag atc att	637
Pro Arg Ile Glu Arg Ala Gly Met Asp Gly Ser Thr Arg Lys Ile Ile	
175 180 185	
gtg gac tcg gac att tac tgg ccc aat gga ctg acc atc gac ctg gag	685
Val Asp Ser Asp Ile Tyr Trp Pro Asn Gly Leu Thr Ile Asp Leu Glu	
190 195 200 205	
gag cag aag ctc tac tgg gct gac gcc aag ctc agc ttc atc cac cgt	733
Glu Gln Lys Leu Tyr Trp Ala Asp Ala Lys Leu Ser Phe Ile His Arg	
210 215 220	
gcc aac ctg gac ggc tcg ttc cgg cag aag gtg gtg gag ggc agc ctg	781
Ala Asn Leu Asp Gly Ser Phe Arg Gln Lys Val Val Glu Gly Ser Leu	
225 230 235	

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Thr His Pro Phe Ala Leu Thr Leu Ser Gly Asp Thr Leu Tyr Trp Thr
240 245 250
gac tgg cag acc cgc tcc atc cat gcc tgc aac aag cgc act ggg ggg 877
Asp Trp Gln Thr Arg Ser Ile His Ala Cys Asn Lys Arg Thr Gly Gly
255 260 265
aag agg aag gag atc ctg agt gcc ctc tac tca ccc atg gac atc cag 925
Lys Arg Lys Glu Ile Leu Ser Ala Leu Tyr Ser Pro Met Asp Ile Gln
270 275 280 285
gtg ctg agc cag gag cgg cag cct ttc ttc cac act cgc tgt gag gag 973
Val Leu Ser Gln Glu Arg Gln Pro Phe Phe His Thr Arg Cys Glu Glu
290 295 300
gac aat ggc ggc tgc tcc cac ctg tgc ctg ctg tcc cca agc gag cct
1021
Asp Asn Gly Gly Cys Ser His Leu Cys Leu Leu Ser Pro Ser Glu Pro
305 310 315
ttc tac aca tgc gcc tgc ccc acg ggt gtg cag ctg cag gac aac ggc
1069
Phe Tyr Thr Cys Ala Cys Pro Thr Gly Val Gln Leu Gln Asp Asn Gly
320 325 330
agg acg tgt aag gca gga gcc gag gag gtg ctg ctg ctg gcc cgg cgg
1117
Arg Thr Cys Lys Ala Gly Ala Glu Glu Val Leu Leu Leu Ala Arg Arg
335 340 345
acg gac cta cgg agg atc tcg ctg gac acg ccg gac ttc acc gac atc
1165
Thr Asp Leu Arg Arg Ile Ser Leu Asp Thr Pro Asp Phe Thr Asp Ile
350 355 360 365
gtg ctg cag gtg gac gac atc cgg cac gcc att gcc atc gac tac gac
1213
Val Leu Gln Val Asp Asp Ile Arg His Ala Ile Ala Ile Asp Tyr Asp

370	375	380	
ccg cta gag ggc tat gtc tac tgg aca gat gac gag gtg cgg gcc atc 1261			
Pro Leu Glu Gly Tyr Val Tyr Trp Thr Asp Asp Glu Val Arg Ala Ile			
385	390	395	
cgc agg gcg tac ctg gac ggg tct ggg gcg cag acg ctg gtc aac acc 1309			
Arg Arg Ala Tyr Leu Asp Gly Ser Gly Ala Gln Thr Leu Val Asn Thr			
400	405	410	
gag atc aac gac ccc gat ggc atc gcg gtc gac tgg gtg gcc cga aac 1357			
Glu Ile Asn Asp Pro Asp Gly Ile Ala Val Asp Trp Val Ala Arg Asn			
415	420	425	
ctc tac tgg acc gac acg ggc acg gac cgc atc gag gtg acg cgc ctc 1405			
Leu Tyr Trp Thr Asp Thr Gly Thr Asp Arg Ile Glu Val Thr Arg Leu			
430	435	440	445
aac ggc acc tcc cgc aag atc ctg gtg tcg gag gac ctg gac gag ccc 1453			
Asn Gly Thr Ser Arg Lys Ile Leu Val Ser Glu Asp Leu Asp Glu Pro			
450	455	460	
cga gcc atc gca ctg cac ccc gtg atg ggc ctc atg tac tgg aca gac 1501			
Arg Ala Ile Ala Leu His Pro Val Met Gly Leu Met Tyr Trp Thr Asp			
465	470	475	
tgg gga gag aac cct aaa atc gag tgt gcc aac ttg gat ggg cag gag 1549			
Trp Gly Glu Asn Pro Lys Ile Glu Cys Ala Asn Leu Asp Gly Gln Glu			
480	485	490	
cgg cgt gtg ctg gtc aat gcc tcc ctc ggg tgg ccc aac ggc ctg gcc 1597			
Arg Arg Val Leu Val Asn Ala Ser Leu Gly Trp Pro Asn Gly Leu Ala			
495	500	505	

ctg gac ctg cag gag ggg aag ctc tac tgg gga gac gcc aag aca gac
1645

Leu Asp Leu Gln Glu Gly Lys Leu Tyr Trp Gly Asp Ala Lys Thr Asp
510 515 520 525

aag atc gag gtg atc aat gtt gat ggg acg aag agg cgg acc ctc ctg
1693

Lys Ile Glu Val Ile Asn Val Asp Gly Thr Lys Arg Arg Thr Leu Leu
530 535 540

gag gac aag ctc ccg cac att ttc ggg ttc acg ctg ctg ggg gac ttc
1741

Glu Asp Lys Leu Pro His Ile Phe Gly Phe Thr Leu Leu Gly Asp Phe
545 550 555

atc tac tgg act gac tgg cag cgc cgc agc atc gag cgg gtg cac aag
1789

Ile Tyr Trp Thr Asp Trp Gln Arg Arg Ser Ile Glu Arg Val His Lys
560 565 570

gtc aag gcc agc cgg gac gtc atc att gac cag ctg ccc gac ctg atg
1837

Val Lys Ala Ser Arg Asp Val Ile Ile Asp Gln Leu Pro Asp Leu Met
575 580 585

ggg ctc aaa gct gtg aat gtg gcc aag gtc gtc gga acc aac ccg tgt
1885

Gly Leu Lys Ala Val Asn Val Ala Lys Val Val Gly Thr Asn Pro Cys
590 595 600 605

gcg gac agg aac ggg ggg tgc agc cac ctg tgc ttc ttc aca ccc cac
1933

Ala Asp Arg Asn Gly Gly Cys Ser His Leu Cys Phe Phe Thr Pro His
610 615 620

gca acc cgg tgt ggc tgc ccc atc ggc ctg gag ctg ctg agt gac atg
1981

Ala Thr Arg Cys Gly Cys Pro Ile Gly Leu Glu Leu Leu Ser Asp Met
625 630 635

aag acc tgc atc gtg cct gag gcc ttc ttg gtc ttc acc agc aga gcc
2029

Lys Thr Cys Ile Val Pro Glu Ala Phe Leu Val Phe Thr Ser Arg Ala

640

645

650

gcc atc cac agg atc tcc ctc gag acc aat aac aac gac gtg gcc atc
2077

Ala Ile His Arg Ile Ser Leu Glu Thr Asn Asn Asn Asp Val Ala Ile

655

660

665

ccg ctc acg ggc gtc aag gag gcc tca gcc ctg gac ttt gat gtg tcc
2125

Pro Leu Thr Gly Val Lys Glu Ala Ser Ala Leu Asp Phe Asp Val Ser

670

675

680

685

aac aac cac atc tac tgg aca gac gtc agc ctg aag acc atc agc cgc
2173

Asn Asn His Ile Tyr Trp Thr Asp Val Ser Leu Lys Thr Ile Ser Arg

690

695

700

gcc ttc atg aac ggg agc tcg gtg gag cac gtg gtg gag ttt ggc ctt
2221

Ala Phe Met Asn Gly Ser Ser Val Glu His Val Val Glu Phe Gly Leu

705

710

715

gac tac ccc gag ggc atg gcc gtt gac tgg atg ggc aag aac ctc tac
2269

Asp Tyr Pro Glu Gly Met Ala Val Asp Trp Met Gly Lys Asn Leu Tyr

720

725

730

tgg gcc gac act ggg acc aac aga atc gaa gtg gcg cgg ctg gac ggg
2317

Trp Ala Asp Thr Gly Thr Asn Arg Ile Glu Val Ala Arg Leu Asp Gly

735

740

745

cag ttc cgg caa gtc ctc gtg tgg agg gac ttg gac aac ccg agg tcg
2365

Gln Phe Arg Gln Val Leu Val Trp Arg Asp Leu Asp Asn Pro Arg Ser

750

755

760

765

ctg gcc ctg gat ccc acc aag ggc tac atc tac tgg acc gag tgg ggc
2413

Leu Ala Leu Asp Pro Thr Lys Gly Tyr Ile Tyr Trp Thr Glu Trp Gly
770 775 780

ggc aag ccg agg atc gtg cgg gcc ttc atg gac ggg acc aac tgc atg
2461

Gly Lys Pro Arg Ile Val Arg Ala Phe Met Asp Gly Thr Asn Cys Met
785 790 795

acg ctg gtg gac aag gtg ggc cgg gcc aac gac ctc acc att gac tac
2509

Thr Leu Val Asp Lys Val Gly Arg Ala Asn Asp Leu Thr Ile Asp Tyr
800 805 810

gct gac cag cgc ctc tac tgg acc gac ctg gac acc aac atg atc gag
2557

Ala Asp Gln Arg Leu Tyr Trp Thr Asp Leu Asp Thr Asn Met Ile Glu
815 820 825

tcg tcc aac atg ctg ggt cag gag cgg gtc gtg att gcc gac gat ctc
2605

Ser Ser Asn Met Leu Gly Gln Glu Arg Val Val Ile Ala Asp Asp Leu
830 835 840 845

ccg cac ccg ttc ggt ctg acg cag tac agc gat tat atc tac tgg aca
2653

Pro His Pro Phe Gly Leu Thr Gln Tyr Ser Asp Tyr Ile Tyr Trp Thr
850 855 860

gac tgg aat ctg cac agc att gag cgg gcc gac aag act agc ggc cgg
2701

Asp Trp Asn Leu His Ser Ile Glu Arg Ala Asp Lys Thr Ser Gly Arg
865 870 875

aac cgc acc ctc atc cag ggc cac ctg gac ttc gtg atg gac atc ctg
2749

Asn Arg Thr Leu Ile Gln Gly His Leu Asp Phe Val Met Asp Ile Leu
880 885 890

gtg ttc cac tcc tcc cgc cag gat ggc ctc aat gac tgt atg cac aac
2797

Val Phe His Ser Ser Arg Gln Asp Gly Leu Asn Asp Cys Met His Asn
895 900 905

aac ggg cag tgt ggg cag ctg tgc ctt gcc atc ccc ggc ggc cac cgc
2845

Asn Gly Gln Cys Gly Gln Leu Cys Leu Ala Ile Pro Gly Gly His Arg
910 915 920 925

tgc ggc tgc gcc tca cac tac acc ctg gac ccc agc agc cgc aac tgc
2893

Cys Gly Cys Ala Ser His Tyr Thr Leu Asp Pro Ser Ser Arg Asn Cys
930 935 940

agc ccg ccc acc acc ttc ttg ctg ttc agc cag aaa tct gcc atc agt
2941

Ser Pro Pro Thr Thr Phe Leu Leu Phe Ser Gln Lys Ser Ala Ile Ser
945 950 955

cgg atg atc ccg gac gac cag cac agc ccg gat ctc atc ctg ccc ctg
2989

Arg Met Ile Pro Asp Asp Gln His Ser Pro Asp Leu Ile Leu Pro Leu
960 965 970

cat gga ctg agg aac gtc aaa gcc atc gac tat gac cca ctg gac aag
3037

His Gly Leu Arg Asn Val Lys Ala Ile Asp Tyr Asp Pro Leu Asp Lys
975 980 985

- ttc atc tac tgg gtg gat ggg cgc cag aac atc aag cga gcc aag gac
3085

- Phe Ile Tyr Trp Val Asp Gly Arg Gln Asn Ile Lys Arg Ala Lys Asp
990 995 1000 1005

gac ggg acc cag ccc ttt gtt ttg acc tct ctg agc caa ggc caa aac
3133

Asp Gly Thr Gln Pro Phe Val Leu Thr Ser Leu Ser Gln Gly Gln Asn
1010 1015 1020

cca gac agg cag ccc cac gac ctc agc atc gac atc tac agc cgg aca
3181

Pro Asp Arg Gln Pro His Asp Leu Ser Ile Asp Ile Tyr Ser Arg Thr

1025

1030

1035

ctg ttc tgg acg tgc gag gcc acc aat acc atc aac gtc cac agg ctg
3229

Leu Phe Trp Thr Cys Glu Ala Thr Asn Thr Ile Asn Val His Arg Leu

1040

1045

1050

agc ggg gaa gcc atg ggg gtg gtg ctg cgt ggg gac cgc gac aag ccc
3277

Ser Gly Glu Ala Met Gly Val Val Leu Arg Gly Asp Arg Asp Lys Pro

1055

1060

1065

agg gcc atc gtc gtc aac gcg gag cga ggg tac ctg tac ttc acc aac
3325

Arg Ala Ile Val Val Asn Ala Glu Arg Gly Tyr Leu Tyr Phe Thr Asn

1070

1075

1080

1085

atg cag gac cgg gca gcc aag atc gaa cgc gca gcc ctg gac ggc acc
3373

Met Gln Asp Arg Ala Ala Lys Ile Glu Arg Ala Ala Leu Asp Gly Thr

1090

1095

1100

gag cgc gag gtc ctc ttc acc acc ggc ctc atc cgc cct gtg gcc ctg
3421

Glu Arg Glu Val Leu Phe Thr Thr Gly Leu Ile Arg Pro Val Ala Leu

1105

1110

1115

- gtg gtg gac aac aca ctg ggc aag ctg ttc tgg gtg gac gcg gac ctg
3469

- Val Val Asp Asn Thr Leu Gly Lys Leu Phe Trp Val Asp Ala Asp Leu

1120

1125

1130

aag cgc att gag agc tgt gac ctg tca ggg gcc aac cgc ctg acc ctg
3517

Lys Arg Ile Glu Ser Cys Asp Leu Ser Gly Ala Asn Arg Leu Thr Leu

1135

1140

1145

gag gac gcc aac atc gtg cag cct ctg ggc ctg acc atc ctt ggc aag
3565

Glu Asp Ala Asn Ile Val Gln Pro Leu Gly Leu Thr Ile Leu Gly Lys
1150 1155 1160 1165

cat ctc tac tgg atc gac cgc cag cag atg atc gag cgt gtg gag
3613

His Leu Tyr Trp Ile Asp Arg Gln Gln Gln Met Ile Glu Arg Val Glu
1170 1175 1180

aag acc acc ggg gac aag cgg act cgc atc cag ggc cgt gtc gcc cac
3661

Lys Thr Thr Gly Asp Lys Arg Thr Arg Ile Gln Gly Arg Val Ala His
1185 1190 1195

ctc act ggc atc cat gca gtg gag gaa gtc agc ctg gag gag ttc tca
3709

Leu Thr Gly Ile His Ala Val Glu Glu Val Ser Leu Glu Glu Phe Ser
1200 1205 1210

gcc cac cca tgt gcc cgt gac aat ggt ggc tgc tcc cac atc tgt att
3757

Ala His Pro Cys Ala Arg Asp Asn Gly Gly Cys Ser His Ile Cys Ile
1215 1220 1225

gcc aag ggt gat ggg aca cca cgg tgc tca tgc cca gtc cac ctc gtg
3805

Ala Lys Gly Asp Gly Thr Pro Arg Cys Ser Cys Pro Val His Leu Val
1230 1235 1240 1245

- ctc ctg cag aac ctg ctg acc tgt gga gag ccg ccc acc tgc tcc ccg
3853

- Leu Leu Gln Asn Leu Leu Thr Cys Gly Glu Pro Pro Thr Cys Ser Pro
1250 1255 1260

gac cag ttt gca tgt gcc aca ggg gag atc gac tgt atc ccc ggg gcc
3901

Asp Gln Phe Ala Cys Ala Thr Gly Glu Ile Asp Cys Ile Pro Gly Ala
1265 1270 1275

tgg cgc tgt gac ggc ttt ccc gag tgc gat gac cag agc gac gag gag
3949

Trp Arg Cys Asp Gly Phe Pro Glu Cys Asp Asp Gln Ser Asp Glu Glu
1280 1285 1290

ggc tgc ccc gtg tgc tcc gcc gcc cag ttc ccc tgc gcg cgg ggt cag
3997

Gly Cys Pro Val Cys Ser Ala Ala Gln Phe Pro Cys Ala Arg Gly Gln
1295 1300 1305

tgt gtg gac ctg cgc ctg cgc tgc gac ggc gag gca gac tgt cag gac
4045

Cys Val Asp Leu Arg Leu Arg Cys Asp Gly Glu Ala Asp Cys Gln Asp
1310 1315 1320 1325

cgc tca gac gag gtg gac tgt gac gcc atc tgc ctg ccc aac cag ttc
4093

Arg Ser Asp Glu Val Asp Cys Asp Ala Ile Cys Leu Pro Asn Gln Phe
1330 1335 1340

cgg tgt gcg agc ggc cag tgt gtc ctc atc aaa cag cag tgc gac tcc
4141

Arg Cys Ala Ser Gly Gln Cys Val Leu Ile Lys Gln Gln Cys Asp Ser
1345 1350 1355

ttc ccc gac tgt atc gac ggc tcc gac gag ctc atg tgt gaa atc acc
4189

Phe Pro Asp Cys Ile Asp Gly Ser Asp Glu Leu Met Cys Glu Ile Thr
1360 1365 1370

- aag ccg ccc tca gac gac agc ccg gcc cac agc agt gcc atc ggg ccc
4237

- Lys Pro Pro Ser Asp Asp Ser Pro Ala His Ser Ser Ala Ile Gly Pro
1375 1380 1385

gtc att ggc atc atc ctc tct ctc ttc gtc atg ggt ggt gtc tat ttt
4285

Val Ile Gly Ile Ile Leu Ser Leu Phe Val Met Gly Gly Val Tyr Phe
1390 1395 1400 1405

gtg tgc cag cgc gtg gtg tgc cag cgc tat gcg ggg gcc aac ggg ccc
4333

Val Cys Gln Arg Val Val Cys Gln Arg Tyr Ala Gly Ala Asn Gly Pro
1410 1415 1420

ttc ccg cac gag tat gtc agc ggg acc ccg cac gtg ccc ctc aat ttc
4381

Phe Pro His Glu Tyr Val Ser Gly Thr Pro His Val Pro Leu Asn Phe
1425 1430 1435

ata gcc ccg ggc ggt tcc cag cat ggc ccc ttc aca ggc atc gca tgc
4429

Ile Ala Pro Gly Gly Ser Gln His Gly Pro Phe Thr Gly Ile Ala Cys
1440 1445 1450

gga aag tcc atg atg agc tcc gtg agc ctg atg ggg ggc cgg ggc ggg
4477

Gly Lys Ser Met Met Ser Ser Val Ser Leu Met Gly Gly Arg Gly Gly
1455 1460 1465

gtg ccc ctc tac gac cgg aac cac gtc aca ggg gcc tcg tcc agc agc
4525

Val Pro Leu Tyr Asp Arg Asn His Val Thr Gly Ala Ser Ser Ser Ser
1470 1475 1480 1485

tcg tcc agc acg aag gcc acg ctg tac ccg ccg atc ctg aac ccg ccg
4573

Ser Ser Ser Thr Lys Ala Thr Leu Tyr Pro Pro Ile Leu Asn Pro Pro
1490 1495 1500

ccc tcc ccg gcc acg gac ccc tcc ctg tac aac atg gac atg ttc tac
4621

Pro Ser Pro Ala Thr Asp Pro Ser Leu Tyr Asn Met Asp Met Phe Tyr
1505 1510 1515

tct tca aac att ccg gcc act gcg aga ccg tac agg ccc tac atc att
4669

Ser Ser Asn Ile Pro Ala Thr Ala Arg Pro Tyr Arg Pro Tyr Ile Ile
1520 1525 1530

cga gga atg gcg ccc ccg acg acg ccc tgc agc acc gac gtg tgt gac
4717

Arg Gly Met Ala Pro Pro Thr Thr Pro Cys Ser Thr Asp Val Cys Asp
1535 1540 1545

agc gac tac agc gcc agc cgc tgg aag gcc agc aag tac tac ctg gat
4765

Ser Asp Tyr Ser Ala Ser Arg Trp Lys Ala Ser Lys Tyr Tyr Leu Asp
1550 1555 1560 1565

ttg aac tcg gac tca gac ccc tat cca ccc cca ccc acg ccc cac agc
4813

Leu Asn Ser Asp Ser Asp Pro Tyr Pro Pro Pro Pro Thr Pro His Ser
1570 1575 1580

cag tac ctg tcg gcg gag gac agc tgc ccg ccc tcg ccc gcc acc gag
4861

Gln Tyr Leu Ser Ala Glu Asp Ser Cys Pro Pro Ser Pro Ala Thr Glu
1585 1590 1595

agg agc tac ttc cat ctc ttc ccg ccc cct ccg tcc ccc tgc acg gac
4909

Arg Ser Tyr Phe His Leu Phe Pro Pro Pro Pro Ser Pro Cys Thr Asp
1600 1605 1610

tca tcc tgacctcggc cgggccactc tggcttctct gtgcccctgt aaatagtttt
4965

Ser Ser

1615

- aaatatgaac aaagaaaaaa atatatttta tgattttaaaa aataaatata attgggattt
5025

- taaaaacatg agaaatgtga actgtgatgg ggtgggcagg gctgggagaa ctttgtacag
5085

tggagaaata tttataaact taattttgta aaaca
5120

<210> 3

<211> 1615

<212> PRT

<213> Homo sapiens

<400> 3

Met Glu Ala Ala Pro Pro Gly Pro Pro Trp Pro Leu Leu Leu Leu Leu

1 5 10 15

Leu Leu Leu Leu Ala Leu Cys Gly Cys Pro Ala Pro Ala Ala Ala Ser

20 25 30

Pro Leu Leu Leu Phe Ala Asn Arg Arg Asp Val Arg Leu Val Asp Ala

35 40 45

Gly Gly Val Lys Leu Glu Ser Thr Ile Val Val Ser Gly Leu Glu Asp

50 55 60

Ala Ala Ala Val Asp Phe Gln Phe Ser Lys Gly Ala Val Tyr Trp Thr

65 70 75 80

Asp Val Ser Glu Glu Ala Ile Lys Gln Thr Tyr Leu Asn Gln Thr Gly

85 90 95

Ala Ala Val Gln Asn Val Val Ile Ser Gly Leu Val Ser Pro Asp Gly

100 105 110

Leu Ala Cys Asp Trp Val Gly Lys Lys Leu Tyr Trp Thr Asp Ser Glu

115 120 125

Thr Asn Arg Ile Glu Val Ala Asn Leu Asn Gly Thr Ser Arg Lys Val

130 135 140

Leu Phe Trp Gln Asp Leu Asp Gln Pro Lys Ala Ile Ala Leu Asp Pro

145 150 155 160

Ala His Gly Tyr Met Tyr Trp Thr Asp Trp Gly Glu Thr Pro Arg Ile

165 170 175

Glu Arg Ala Gly Met Asp Gly Ser Thr Arg Lys Ile Ile Val Asp Ser

180 185 190

Asp Ile Tyr Trp Pro Asn Gly Leu Thr Ile Asp Leu Glu Glu Gln Lys

195	200	205
Leu Tyr Trp Ala Asp Ala Lys Leu Ser Phe Ile His Arg Ala Asn Leu		
210	215	220
Asp Gly Ser Phe Arg Gln Lys Val Val Glu Gly Ser Leu Thr His Pro		
225	230	235
Phe Ala Leu Thr Leu Ser Gly Asp Thr Leu Tyr Trp Thr Asp Trp Gln		
245	250	255
Thr Arg Ser Ile His Ala Cys Asn Lys Arg Thr Gly Gly Lys Arg Lys		
260	265	270
Glu Ile Leu Ser Ala Leu Tyr Ser Pro Met Asp Ile Gln Val Leu Ser		
275	280	285
Gln Glu Arg Gln Pro Phe Phe His Thr Arg Cys Glu Glu Asp Asn Gly		
290	295	300
Gly Trp Ser His Leu Cys Leu Leu Ser Pro Ser Glu Pro Phe Tyr Thr		
305	310	315
Cys Ala Cys Pro Thr Gly Val Gln Met Gln Asp Asn Gly Arg Thr Cys		
325	330	335
Lys Ala Gly Ala Glu Glu Val Leu Leu Leu Ala Arg Arg Thr Asp Leu		
340	345	350
Arg Arg Ile Ser Leu Asp Thr Pro Asp Phe Thr Asp Ile Val Leu Gln		
355	360	365
Val Asp Asp Ile Arg His Ala Ile Ala Ile Asp Tyr Asp Pro Leu Glu		
370	375	380
Gly Tyr Val Tyr Trp Thr Asp Asp Glu Val Arg Ala Ile Arg Arg Ala		
385	390	395
Tyr Leu Asp Gly Ser Gly Ala Gln Thr Leu Val Asn Thr Glu Ile Asn		
405	410	415
Asp Pro Asp Gly Ile Ala Val Asp Trp Val Ala Arg Asn Leu Tyr Trp		
420	425	430

Thr Asp Thr Gly Thr Asp Arg Ile Glu Val Thr Arg Leu Asn Gly Thr
 435 440 445
 Ser Arg Lys Ile Leu Val Ser Glu Asp Leu Asp Glu Pro Arg Ala Ile
 450 455 460
 Ala Leu His Pro Val Met Gly Leu Met Tyr Trp Thr Asp Trp Gly Glu
 465 470 475 480
 Asn Pro Lys Ile Glu Cys Ala Asn Leu Asp Gly Gln Glu Arg Arg Val
 485 490 495
 Leu Val Asn Ala Ser Leu Gly Trp Pro Asn Gly Leu Ala Leu Asp Leu
 500 505 510
 Gln Glu Gly Lys Leu Tyr Trp Gly Asp Ala Lys Thr Asp Lys Ile Glu
 515 520 525
 Val Ile Asn Val Asp Gly Thr Lys Arg Arg Thr Leu Leu Glu Asp Lys
 530 535 540
 Leu Pro His Ile Phe Gly Phe Thr Leu Leu Gly Asp Phe Ile Tyr Trp
 545 550 555 560
 Thr Asp Trp Gln Arg Arg Ser Ile Glu Arg Val His Lys Val Lys Ala
 565 570 575
 Ser Arg Asp Val Ile Ile Asp Gln Leu Pro Asp Leu Met Gly Leu Lys
 580 585 590
 Ala Val Asn Val Ala Lys Val Val Gly Thr Asn Pro Cys Ala Asp Arg
 595 600 605
 Asn Gly Gly Cys Ser His Leu Cys Phe Phe Thr Pro His Ala Thr Arg
 610 615 620
 Cys Gly Cys Pro Ile Gly Leu Glu Leu Leu Ser Asp Met Lys Thr Cys
 625 630 635 640
 Ile Val Pro Glu Ala Phe Leu Val Phe Thr Ser Arg Ala Ala Ile His
 645 650 655
 Arg Ile Ser Leu Glu Thr Asn Asn Asn Asp Val Ala Ile Pro Leu Thr

660	665	670	
Gly Val Lys Glu Ala Ser Ala Leu Asp Phe Asp Val Ser Asn Asn His			
675	680	685	
Ile Tyr Trp Thr Asp Val Ser Leu Lys Asn Ile Ser Arg Ala Phe Met			
690	695	700	
Asn Gly Ser Ser Val Glu His Val Val Glu Phe Gly Leu Asp Tyr Pro			
705	710	715	720
Glu Gly Met Ala Val Asp Trp Met Gly Lys Asn Leu Tyr Trp Ala Asp			
725	730	735	
Thr Gly Thr Asn Arg Ile Glu Val Ala Arg Leu Asp Gly Gln Phe Arg			
740	745	750	
Gln Val Leu Val Trp Arg Asp Leu Asp Asn Pro Arg Ser Leu Ala Leu			
755	760	765	
Asp Pro Thr Lys Gly Tyr Ile Tyr Trp Thr Glu Trp Gly Gly Lys Pro			
770	775	780	
Arg Ile Val Arg Ala Phe Met Asp Gly Thr Asn Cys Met Thr Leu Val			
785	790	795	800
Asp Lys Val Gly Arg Ala Asn Asp Leu Thr Ile Asp Tyr Ala Asp Gln			
805	810	815	
Arg Leu Tyr Trp Thr Asp Leu Asp Thr Asn Met Ile Glu Ser Ser Asn			
820	825	830	
Met Leu Gly Gln Glu Arg Val Val Ile Ala Asp Asp Leu Pro His Pro			
835	840	845	
Phe Gly Leu Thr Gln Tyr Ser Asp Tyr Ile Tyr Trp Thr Asp Trp Asn			
850	855	860	
Leu His Ser Ile Glu Arg Ala Asp Lys Thr Ser Gly Arg Asn Arg Thr			
865	870	875	880
Leu Ile Gln Gly His Leu Asp Phe Val Met Asp Ile Leu Val Phe His			
885	890	895	

Ser Ser Arg Gln Asp Gly Leu Asn Asp Cys Met His Asn Asn Gly Gln
 900 905 910
 Cys Gly Gln Leu Cys Leu Ala Ile Pro Gly Gly His Arg Cys Gly Cys
 915 920 925
 Ala Ser His Tyr Thr Leu Asp Pro Ser Ser Arg Asn Cys Ser Pro Pro
 930 935 940
 Thr Thr Phe Leu Leu Phe Ser Gln Lys Ser Ala Ile Ser Arg Met Ile
 945 950 955 960
 Pro Asp Asp Gln His Ser Pro Asp Leu Ile Leu Pro Leu His Gly Leu
 965 970 975
 Arg Asn Val Lys Ala Ile Asp Tyr Asp Pro Leu Asp Lys Phe Ile Tyr
 980 985 990
 Trp Val Asp Gly Arg Gln Asn Ile Lys Arg Ala Lys Asp Asp Gly Thr
 995 1000 1005
 Gln Pro Phe Val Leu Thr Ser Leu Ser Gln Gly Gln Asn Pro Asp Arg
 1010 1015 1020
 Gln Pro His Asp Leu Ser Ile Asp Ile Tyr Ser Arg Thr Leu Phe Trp
 1025 1030 1035 1040
 Thr Cys Glu Ala Thr Asn Thr Ile Asn Val His Arg Leu Ser Gly Glu
 1045 1050 1055
 Ala Met Gly Val Val Leu Arg Gly Asp Arg Asp Lys Pro Arg Ala Ile
 1060 1065 1070
 Val Val Asn Ala Glu Arg Gly Tyr Leu Tyr Phe Thr Asn Met Gln Asp
 1075 1080 1085
 Arg Ala Ala Lys Ile Glu Arg Ala Ala Leu Asp Gly Thr Glu Arg Glu
 1090 1095 1100
 Val Leu Phe Thr Thr Gly Leu Ile Arg Pro Val Ala Leu Val Val Asp
 1105 1110 1115 1120
 Asn Thr Leu Gly Lys Leu Phe Trp Val Asp Ala Asp Leu Lys Arg Ile

1125	1130	1135	
Glu Ser Cys Asp Leu Ser Gly Ala Asn Arg Leu Thr Leu Glu Asp Ala			
1140	1145	1150	
Asn Ile Val Gln Pro Leu Gly Leu Thr Ile Leu Gly Lys His Leu Tyr			
1155	1160	1165	
Trp Ile Asp Arg Gln Gln Gln Met Ile Glu Arg Val Glu Lys Thr Thr			
1170	1175	1180	
Gly Asp Lys Arg Thr Arg Ile Gln Gly Arg Val Ala His Leu Thr Gly			
1185	1190	1195	1200
Ile His Ala Val Glu Glu Val Ser Leu Glu Glu Phe Ser Ala His Pro			
1205	1210	1215	
Cys Ala Arg Asp Asn Gly Gly Cys Ser His Ile Cys Ile Ala Lys Gly			
1220	1225	1230	
Asp Gly Thr Pro Arg Cys Ser Cys Pro Val His Leu Val Leu Leu Gln			
1235	1240	1245	
Asn Leu Leu Thr Cys Gly Glu Pro Pro Thr Cys Ser Pro Asp Gln Phe			
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Ala Cys Ala Thr Gly Glu Ile Asp Cys Ile Pro Gly Ala Trp Arg Cys			
1265	1270	1275	1280
Asp Gly Phe Pro Glu Cys Asp Asp Gln Ser Asp Glu Glu Gly Cys Pro			
1285	1290	1295	
Val Cys Ser Ala Ala Gln Phe Pro Cys Ala Arg Gly Gln Cys Val Asp			
1300	1305	1310	
Leu Arg Leu Arg Cys Asp Gly Glu Ala Asp Cys Gln Asp Arg Ser Asp			
1315	1320	1325	
Glu Val Asp Cys Asp Ala Ile Cys Leu Pro Asn Gln Phe Arg Cys Ala			
1330	1335	1340	
Ser Gly Gln Cys Val Leu Ile Lys Gln Gln Cys Asp Ser Phe Pro Asp			
1345	1350	1355	1360

Cys Ile Asp Gly Ser Asp Glu Leu Met Cys Glu Ile Thr Lys Pro Pro			
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Ser Asp Asp Ser Pro Ala His Ser Ser Ala Ile Gly Pro Val Ile Gly			
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Ile Ile Leu Ser Leu Phe Val Met Gly Gly Val Tyr Phe Val Cys Gln			
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Arg Val Val Cys Gln Arg Tyr Ala Gly Ala Asn Gly Pro Phe Pro His			
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Glu Tyr Val Ser Gly Thr Pro His Val Pro Leu Asn Phe Ile Ala Pro			
1425	1430	1435	1440
Gly Gly Ser Gln His Gly Pro Phe Thr Gly Ile Ala Cys Gly Lys Ser			
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Met Met Ser Ser Val Ser Leu Met Gly Gly Arg Gly Gly Val Pro Leu			
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Tyr Asp Arg Asn His Val Thr Gly Ala Ser Ser Ser Ser Ser Ser Ser			
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Thr Lys Ala Thr Leu Tyr Pro Pro Ile Leu Asn Pro Pro Pro Ser Pro			
1490	1495	1500	
Ala Thr Asp Pro Ser Leu Tyr Asn Met Asp Met Phe Tyr Ser Ser Asn			
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Ile Pro Ala Thr Ala Arg Pro Tyr Arg Pro Tyr Ile Ile Arg Gly Met			
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Ala Pro Pro Thr Thr Pro Cys Ser Thr Asp Val Cys Asp Ser Asp Tyr			
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Ser Ala Ser Arg Trp Lys Ala Ser Lys Tyr Tyr Leu Asp Leu Asn Ser			
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Asp Ser Asp Pro Tyr Pro Pro Pro Pro Thr Pro His Ser Gln Tyr Leu			
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Phe His Leu Phe Pro Pro Pro Pro Ser Pro Cys Thr Asp Ser Ser

1605 1610 1615

<210> 4

<211> 1615

<212> PRT

<213> Homo sapiens

<400> 4

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Pro Leu Leu Leu Phe Ala Asn Arg Arg Asp Val Arg Leu Val Asp Ala

35 40 45

Gly Gly Val Lys Leu Glu Ser Thr Ile Val Val Ser Gly Leu Glu Asp

50 55 60

Ala Ala Ala Val Asp Phe Gln Phe Ser Lys Gly Ala Val Tyr Trp Thr

65 70 75 80

Asp Val Ser Glu Glu Ala Ile Lys Gln Thr Tyr Leu Asn Gln Thr Gly

85 90 95

Ala Ala Val Gln Asn Val Val Ile Ser Gly Leu Val Ser Pro Asp Gly

100 105 110

Leu Ala Cys Asp Trp Val Gly Lys Lys Leu Tyr Trp Thr Asp Ser Glu

115 120 125

Thr Asn Arg Ile Glu Val Ala Asn Leu Asn Gly Thr Ser Arg Lys Val

130 135 140

Leu Phe Trp Gln Asp Leu Asp Gln Pro Lys Ala Ile Ala Leu Asp Pro
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 Ala His Gly Tyr Met Tyr Trp Thr Asp Trp Val Glu Thr Pro Arg Ile
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 Asp Ile Tyr Trp Pro Asn Gly Leu Thr Ile Asp Leu Glu Glu Gln Lys
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 Leu Tyr Trp Ala Asp Ala Lys Leu Ser Phe Ile His Arg Ala Asn Leu
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 Asp Gly Ser Phe Arg Gln Lys Val Val Glu Gly Ser Leu Thr His Pro
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 Phe Ala Leu Thr Leu Ser Gly Asp Thr Leu Tyr Trp Thr Asp Trp Gln
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 Thr Arg Ser Ile His Ala Cys Asn Lys Arg Thr Gly Gly Lys Arg Lys
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 Arg Arg Ile Ser Leu Asp Thr Pro Asp Phe Thr Asp Ile Val Leu Gln
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 Val Asp Asp Ile Arg His Ala Ile Ala Ile Asp Tyr Asp Pro Leu Glu

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Tyr Leu Asp Gly Ser Gly Ala Gln Thr Leu Val Asn Thr Glu Ile Asn			
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Ser Arg Lys Ile Leu Val Ser Glu Asp Leu Asp Glu Pro Arg Ala Ile			
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Asn Pro Lys Ile Glu Cys Ala Asn Leu Asp Gly Gln Glu Arg Arg Val			
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Leu Val Asn Ala Ser Leu Gly Trp Pro Asn Gly Leu Ala Leu Asp Leu			
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Gln Glu Gly Lys Leu Tyr Trp Gly Asp Ala Lys Thr Asp Lys Ile Glu			
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Val Ile Asn Val Asp Gly Thr Lys Arg Arg Thr Leu Leu Glu Asp Lys			
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Leu Pro His Ile Phe Gly Phe Thr Leu Leu Gly Asp Phe Ile Tyr Trp			
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Thr Asp Trp Gln Arg Arg Ser Ile Glu Arg Val His Lys Val Lys Ala			
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Ser Arg Asp Val Ile Ile Asp Gln Leu Pro Asp Leu Met Gly Leu Lys			
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Asn Gly Gly Cys Ser His Leu Cys Phe Phe Thr Pro His Ala Thr Arg
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 625 630 635 640
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 645 650 655
 Arg Ile Ser Leu Glu Thr Asn Asn Asn Asp Val Ala Ile Pro Leu Thr
 660 665 670
 Gly Val Lys Glu Ala Ser Ala Leu Asp Phe Asp Val Ser Asn Asn His
 675 680 685
 Ile Tyr Trp Thr Asp Val Ser Leu Lys Asn Ile Ser Arg Ala Phe Met
 690 695 700
 Asn Gly Ser Ser Val Glu His Val Val Glu Phe Gly Leu Asp Tyr Pro
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 785 790 795 800
 Asp Lys Val Gly Arg Ala Asn Asp Leu Thr Ile Asp Tyr Ala Asp Gln
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 Arg Leu Tyr Trp Thr Asp Leu Asp Thr Asn Met Ile Glu Ser Ser Asn
 820 825 830
 Met Leu Gly Gln Glu Arg Val Val Ile Ala Asp Asp Leu Pro His Pro

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Leu His Ser Ile Glu Arg Ala Asp Lys Thr Ser Gly Arg Asn Arg Thr		
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Leu Ile Gln Gly His Leu Asp Phe Val Met Asp Ile Leu Val Phe His		
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Ser Ser Arg Gln Asp Gly Leu Asn Asp Cys Met His Asn Asn Gly Gln		
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Cys Gly Gln Leu Cys Leu Ala Ile Pro Gly Gly His Arg Cys Gly Cys		
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Ala Ser His Tyr Thr Leu Asp Pro Ser Ser Arg Asn Cys Ser Pro Pro		
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Thr Thr Phe Leu Leu Phe Ser Gln Lys Ser Ala Ile Ser Arg Met Ile		
945	950	955
Pro Asp Asp Gln His Ser Pro Asp Leu Ile Leu Pro Leu His Gly Leu		
965	970	975
Arg Asn Val Lys Ala Ile Asp Tyr Asp Pro Leu Asp Lys Phe Ile Tyr		
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Trp Val Asp Gly Arg Gln Asn Ile Lys Arg Ala Lys Asp Asp Gly Thr		
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Gln Pro Phe Val Leu Thr Ser Leu Ser Gln Gly Gln Asn Pro Asp Arg		
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Gln Pro His Asp Leu Ser Ile Asp Ile Tyr Ser Arg Thr Leu Phe Trp		
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Tyr Asp Arg Asn His Val Thr Gly Ala Ser Ser Ser Ser Ser Ser Ser		
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Thr Lys Ala Thr Leu Tyr Pro Pro Ile Leu Asn Pro Pro Pro Ser Pro		
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Ala Pro Pro Thr Thr Pro Cys Ser Thr Asp Val Cys Asp Ser Asp Tyr

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1545

1550

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1560

1565

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1570

1575

1580

Ser Ala Glu Asp Ser Cys Pro Pro Ser Pro Ala Thr Glu Arg Ser Tyr

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1605

1610

1615

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<212> DNA

<213> Homo sapiens

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A1
CONT.

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23

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<400> 28

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56

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<213> Artificial Sequence

<220>

<223> Artificial sequence is a primer.

<400> 36

agctgctcgt agctgtctct ccctgga

27

<210> 37

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Artificial sequence is a primer.

<400> 37

gccgtaatgc ggcacaggga ataagct

27

<210> 38

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Artificial sequence is a primer.

<400> 38

gagaggctat atccctgggc

20

<210> 39

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

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CONT.

<223> Artificial sequence is a primer.

<400> 39

acagcacgtg tttaaagggg

20

<210> 40

<211> 163

<212> DNA

<213> Homo sapiens

<400> 40

actaaagcgc	cgccgcccgc	ccatggagcc	cgagtgaact	cgccgcccgc	ccgtccggcc	60
gccggacaac	atggaggcag	ctccgcccgc	gccgcccgtg	ccgtgctgct	tgctgctgct	120
gctgctgctg	gcgtgtgctg	gctgcccgcg	ccccgcccgc	gcc		163

<210> 41

<211> 419

<212> DNA

<213> Homo sapiens

<400> 41

gccccacagc	ctcgccgctc	ctgctatttg	ccaaccgccc	ggacgtacgg	ctggtggacg	60
ccggcggagt	caagctggag	tccaccatcg	tggtcagcgg	cctggaggat	gcggccgcag	120
tggacttcca	gttttccaag	ggagccgtgt	actggacaga	cgtgagcgag	gaggccatca	180
agcagacctc	cctgaaccag	acggggggccg	ccgtgcagaa	cgtggtcac	tccggcctgg	240
tctctcccga	cggcctcgcc	tgcgactggg	tgggcaagaa	gctgtactgg	acggactcag	300
agaccaaccg	catcgagggtg	gccaacctca	atggcacatc	ccggaagggtg	ctcttctggc	360
aggaccttga	ccagccgagg	gccatcgcc	tggaacccgc	tcacgggtaa	accctgctg	419

<210> 42

<211> 221

<212> DNA

<213> Homo sapiens

<400> 42

ccccgtcaca	ggtacatgta	ctggacagac	tggggtgaga	cgccccggat	tgagcgggca	60
gggatggatg	gcagcaccgc	gaagatcatt	gtggactcgg	acatttactg	gccaatgga	120
ctgaccatcg	acctggagga	gcagaagctc	tactgggctg	acgccaagct	cagcttcac	180
caccgtgcca	acctggacgg	ctcgttccgg	taggtaccca	c		221

<210> 43

<211> 221

<212> DNA

<213> Homo sapiens

<400> 43

tccctgactg	caggcagaag	gtggtggagg	gcagcctgac	gcaccccttc	gccctgacgc	60
tctccgggga	cactctgtac	tggacagact	ggcagaccgc	ctccatccat	gccctgcaaca	120
agcgactgg	ggggaagagg	aaggagatcc	tgagtgcctt	atactacccc	atggacatcc	180
agggtgctgag	ccaggagcgg	cagccttttt	gtgagtgcgc	g		221

<210> 44

<211> 156

<212> DNA

<213> Homo sapiens

<400> 44

tttctcagtc	cacactcgct	gtgaggagga	caatggcggc	tggtcccacc	tgtgcctgct	60
gtccccaagc	gagccttttt	acacatgcgc	ctgccccacg	ggtgtgcaga	tgcaggacaa	120
cggcaggacg	tgtaaggcag	gtgaggcggt	gggacg			156

<210> 45

<211> 416

<212> DNA

<213> Homo sapiens

<400> 45

ctccacagga	gccgaggagg	tgctgctgct	ggccccggcg	acggacctac	ggaggatctc	60
gctggacacg	ccggaactta	ccgacatcgt	gctgcagggtg	gacgacatcc	ggcacgccat	120
tgccatcgac	tacgaccgcg	tagagggcta	tgtctactgg	acagatgacg	agggtgcgggc	180
catccgcagg	gcgtacctgg	acgggtctgg	ggcgacagacg	ctggtcaaca	ccgagatcaa	240
cgaccccgat	ggcatcgcg	tcgactgggt	ggccccgaaac	ctctactgga	ccgacacggg	300
cacggaccgc	atcgagggtga	cgcgcctcaa	cggcacctcc	cgcaagatcc	tgggtgtcgga	360
ggacctggac	gagccccgag	ccatcgact	gcaccccgtg	atggggtaag	acgggc	416

<210> 46

<211> 198

<212> DNA

<213> Homo sapiens

<400> 46

ttcttctcca	gcctcatgta	ctggacagac	tggggagaga	accctaaaat	cgagtgtgcc	60
aacttgatg	ggcaggagcg	gcgtgtgctg	gtcaatgcct	ccctcgggtg	gccccacggc	120
ctggccctgg	acctgcagga	ggggaagctc	tactggggag	acgccaagac	agacaagatc	180
gaggtgaggc	tcctgtgg					198

<210> 47

<211> 244

<212> DNA

<213> Homo sapiens

<400> 47

ccgtcctgca	ggtgatcaat	gttgatggga	cgaagaggcg	gaccctcctg	gaggacaagc	60
tcccgacat	tttcgggttc	acgctgctgg	gggacttcat	ctactggact	gactggcagc	120
gccgcagcat	cgagcgggtg	cacaaggtca	aggccagccg	ggacgtcatc	attgaccagc	180
tgcccgaacct	gatggggctc	aaagctgtga	atgtggccaa	ggtcgtcggg	gagtccgggg	240
ggtc						244

<210> 48

<211> 313

<212> DNA

<213> Homo sapiens

<400> 48

gttcgcttcc	aggaaccaac	ccgtgtgcgg	acaggaacgg	gggggtgcagc	cacctgtgct	60
tctgcacacc	ccacgcaacc	cggtgtggct	gccccatcgg	cctggagctg	ctgagtgaca	120
tgaagacctg	catcgtgcct	gaggcctttt	tggctctcac	cagcagagcc	gccatccaca	180
ggatctccct	cgagaccaat	aacaacgacg	tggccatccc	gctcacgggc	gtcaaggagg	240
cctcagccct	ggactttgat	gtgtccaaca	accacatcta	ctggacagac	gtcagcctga	300
aggtagcgtg	ggc					313

<210> 49

<211> 255

<212> DNA

<213> Homo sapiens

<400> 49

cctgctgcca	gaccatcagc	cgcgcttca	tgaacgggag	ctcgggtggag	cacgtggtgg	60
agtttgccct	tgactacccc	gagggcatgg	ccgttgactg	gatgggcaag	aacctctact	120
gggccgacac	tgggaccaac	agaatcgaag	tggcgcggt	ggacgggcag	ttccggcaag	180
tcctcgtgtg	gagggacttg	gacaacccga	ggtcgctggc	cctggatccc	accaaggggt	240
aagtgtttgc	ctgtc					255

<210> 50

<211> 210

<212> DNA

<213> Homo sapiens

<400> 50
 gtgccttcca gctacatcta ctggaccgag tggggcggca agccgaggat cgtgcggggc 60
 ttcattggacg ggaccaactg catgacgctg gtggacaagg tgggccgggc caacgacctc 120
 accattgact acgctgacca gcgcctctac tggaccgacc tggacaccaa catgatcgag 180
 tcgtccaaca tgctgggtga gggccgggct 210

<210> 51

<211> 352

<212> DNA

<213> Homo sapiens

A'
 CONT.
 <400> 51
 gtgttcatgc aggtcaggag cgggtcgtga ttgccgacga tctcccgcac ccgttcggtc 60
 tgacgcagta cagcgattat atctactgga cagactggaa tctgcacagc attgagcggg 120
 ccgacaagac tagcggcgcg aaccgcaccc tcatccaggg ccacctggac ttcgtgatgg 180
 acatcctggt gttccactcc tcccggcagg atggcctcaa tgactgtatg cacaacaacg 240
 ggcagtgtgg gcagctgtgc cttgccatcc ccggcggcca ccgctgcggc tgcgcctcac 300
 actacacctt ggaccccagc agccgcaact gcagccgtaa gtgcctcatg gt 352

<210> 52

<211> 225

<212> DNA

<213> Homo sapiens

<400> 52
 gcctcctcta cgcccaccac cttcttctgtg ttcagccaga aatctgccat cagtccgatg 60
 atcccggacg accagcacag ccgggatctc atcctgcccc tgcattggact gaggaacgctc 120
 aaagccatcg actatgaccc actggacaag ttcattctact gggtaggatg gcgccagaac 180
 atcaagcgag ccaaggacga cgggacccag gcaggtgccc tgtgg 225

<210> 53

<211> 235

<212> DNA

<213> Homo sapiens

<400> 53
 ctttgtctta cagccctttg ttttgacctc tctgagccaa ggccaaaacc cagacaggca 60
 gccccacgac ctcagcatcg acatctacag ccggacactg ttctggacgt gcgaggccac 120
 caataccatc aacgtccaca ggctgagcgg ggaagccatg ggggtgggtg tgcgtgggga 180
 ccgcgacaag cccaggggca tcgtcgtcaa cgcggagcga gggtaggagg ccaac 235

<210> 54

<211> 218

<212> DNA

<213> Homo sapiens

<400> 54

ccaccctccc	gcaggtacct	gtacttcacc	aacatgcagg	accgggcagc	caagatcgaa	60
cgcgcagccc	tggacggcac	cgagcgcgag	gtcctcttca	ccaccggcct	catccgccct	120
gtggccctgg	tgggtggaaa	cacactgggc	aagctgttct	gggtggacgc	ggacctgaag	180
cgattgaga	gctgtgacct	gtcaggtacg	cgccccgg			218

<210> 55

<211> 234

<212> DNA

<213> Homo sapiens

<400> 55

ggctgcttgc	agggggccaac	cgcctgacct	tggaggacgc	caacatcgtg	cagcctctgg	60
gcctgaccat	ccttggcaag	catctctact	ggatcgaccg	ccagcagcag	atgatcgagc	120
gtgtggagaa	gaccaccggg	gacaagcgga	ctcgcatcca	gggccgtgtc	gcccacctca	180
ctggcatcca	tgcagtggag	gaagtcagcc	tggaggagtt	ctgtacgtgg	gggc	234

<210> 56

<211> 157

<212> DNA

<213> Homo sapiens

<400> 56

ttgtctttgc	agcagcccac	ccatgtgccc	gtgacaatgg	tggtgtctcc	cacatctgta	60
ttgccaaagg	tgatgggaca	ccacgggtgt	catgcccagt	ccacctcgtg	ctcctgcaga	120
acctgctgac	ctgtggaggt	aggtgtgacc	taggtgc			157

<210> 57

<211> 272

<212> DNA

<213> Homo sapiens

<400> 57

gttctcctct	gtccctcccc	cagagccgcc	cacctgtctc	cgggaccagt	ttgcatgtgc	60
cacaggggag	atcgactgta	tccccggggc	ctggcgctgt	gacggctttc	ccgagtgcga	120
tgaccagagc	gacgaggagg	gctgccccgt	gtgtcccgcc	gcccagttcc	cctgcgcgcg	180
gggtcagtgt	gtggacctgc	gctgcgctg	cgacggcgag	gcagactgtc	aggaccgctc	240
agacgaggtg	gactgtgacg	gtgaggccct	cc			272

<210> 58

<211> 134

<212> DNA

<213> Homo sapiens

<400> 58

tctccttgca gccatctgcc tgcccaacca gttccggtgt gcgagcggcc agtgtgtcct	60
catcaaacag cagtgcgact ccttccccga ctgtatcgac ggctccgacg agtcatgtg	120
tggtgagcca gctt	134

<210> 59

<211> 274

<212> DNA

<213> Homo sapiens

<400> 59

gtttgtctct ggcagaaatc accaagccgc cctcagacga cagcccggcc cacagcagtg	60
ccatcggggc cgtcattggc atcatcctct ctctcttcgt catgggtggg gtctatatttg	120
tgtgccagcg cgtgggtgtgc cagcgctatg cgggggccaa cggggcccttc ccgcacgagt	180
atgtcagcgg gacccccgac gtgccccctca atttcatagc cccgggcggt tcccagcatg	240
gcccccttcac aggtaaggag cctgagatat ggaa	274

<210> 60

<211> 164

<212> DNA

<213> Homo sapiens

<400> 60

cttccttgcc aggcacgcga tgcggaaagt ccatgatgag ctccgtgagc ctgatggggg	60
gccccggcgg ggtgcccctc tacgaccgga accacgtcac aggggcctcg tccagcagct	120
cgtccagcac gaaggccacg ctgtaccgcg cgggtgagggg cggg	164

<210> 61

<211> 130

<212> DNA

<213> Homo sapiens

<400> 61

ttggctctcc tcagatcctg aaccgcgcgc cctccccggc cacggacccc tccctgtaca	60
acatggacat gttctactct tcaaacattc cggccactgc gagaccgtac aggtaggaca	120
tccccctgac	130

<210> 62

<211> 496

<212> DNA

<213> Homo sapiens

<400> 62

tcaaacattc	cggccactgc	gagaccgtac	aggccctaca	tcattcgagg	aatggcgccc	60
ccgacgacgc	cctgcagcac	cgacgtgtgt	gacagcgact	acagcgccag	ccgctggaag	120
gccagcaagt	actacctgga	tttgaactcg	gactcagacc	cctatccacc	cccacccacg	180
ccccacagcc	agtacctgtc	ggcggaggac	agctgcccgc	cctcgcccgc	caccgagagg	240
agctacttcc	atctcttccc	gccccctccg	tccccctgca	cggactcatc	ctgacctcgg	300
ccggggccact	ctggcttctc	tgtgcccctg	taaatagttt	taaatatgaa	caaagaaaaa	360
aatatatttt	atgatttaaa	aaataaatat	aattgggatt	ttaaaaacat	gagaaatgtg	420
aactgtgatg	gggtgggcag	ggctggggaga	actttgtaca	gtggagaaat	atttataaac	480
ttaattttgt	aaaaca					496